

CB

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/857,669

DATE: 10/26/2001

TIME: 16:22:19

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\10262001\I857669.raw

ENTERED

4 <110> APPLICANT: Ruelle, Jean-Louis
6 <120> TITLE OF INVENTION: Polypeptides and Polynucleotides
7 "BASB040" From Neisseria Meningitidis and Vaccine Comprising
8 Said Polypeptides and Polynucleotides
11 <130> FILE REFERENCE: BM45339
13 <140> CURRENT APPLICATION NUMBER: 09/857,669
C--> 14 <141> CURRENT FILING DATE: 2001-09-21
16 <150> PRIOR APPLICATION NUMBER: 9826886.5
17 <151> PRIOR FILING DATE: 1998-12-07
19 <150> PRIOR APPLICATION NUMBER: PCT/EP99/09560
20 <151> PRIOR FILING DATE: 1999-12-02
22 <160> NUMBER OF SEQ ID NOS: 11
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 1830
28 <212> TYPE: DNA
29 <213> ORGANISM: Neisseria meningitidis
31 <400> SEQUENCE: 1

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33	gcgcctgcgc cgcaccttc cgaaaacaag gggcggggtt tcgcattggt caaaaacaaa	120
34	agccccgaca cgaatcagt taaattaaaa cccaaattcc ccgtccgcac cgacacgcag	180
35	gatagtgaaa tcaaagatat ggtcgaagaa cacctgccgc tcatcacgca gcagcaggaa	240
36	gaagtattgg acaaggaaca gacgggcttc ctgcgccgaag aagcaccgga caacgttaaa	300
37	accatgctcc gcagcaaagg ctatttcagc agcaaagtca gcctgacgga aaaagacgga	360
38	gcttatacgg tacacatcac accggggccc cgcaccaaaa tcgccaacgt cgggtgcgcc	420
39	atcctcggcg acatcctttc agacggcaac ctgcgcgaat actaccgcaa cgcgctggaa	480
40	aactggcagc agccggtagg cagtgaattc gatcaggaca gttgggaaaa cagcaaaact	540
41	tccgtcctcg gcgcggtaac gcgaaaaggc taccgcgttg ccaagctcgg caacaccg	600
42	gcggccgtca accccgatac cgccaccgtc gatttgaacg tcgtcgtgga cagcggccgc	660
43	cccatacgct tcggcgactt tgaaatcacc ggcacacagc gttaccccga acaaatcgtc	720
44	tccggcctgg cgcgcttcca accgggcacg ccctacgacc tcgacctgct gctcgacttc	780
45	caacaggcac tcgaacaaaa cgggcattat tccggcgcggt ccgtacaagc cgacttcgac	840
46	cgtctccaag gcgaccgcgt ccccgtaaaa gtcagcgtaa ccgaggtcaa acgccacaag	900
47	ctcgaaaccg gcatccgcct cgattcggaa tacggtttg ggcggcaaat cgcctacgac	960
48	tattacaacc tcttcaacaa aggtatatc ggctcggctg tctgggatat ggacaaatac	1020
49	gaaaccacgc ttgcgcggc catcagccag ccgcgcaact atcggggcaa ctactggaca	1080
50	agcaacgttt cctacaaccg ttcgaccacc caaaacctcg aaaaacgcgc cttctccggc	1140
51	ggcatctggt atgtgcgcga ccgcgcgggc atcgatgcca ggcgtggggc agagtttctc	1200
52	gcagaaggcc ggaaaatccc cggctcggat atcgatttg gcaacagcca cgccacgatg	1260
53	ctgaccgcct cttggaaacg ccagctgctc aacaacgtgc tgcattcccga aaacggccat	1320
54	tacctcgacg gcaaaatcgg tacgactttg ggcacatttc tgctctccac cgcgctgatc	1380
55	cgcacctctg cccgtgcagg ttatttcttc acgcccgaaa acaaaaaact cggcacgttc	1440
56	atcatacgcg gacaagcggg ttacaccgtt gcccgcgaca atgccgacgt tccttcaggg	1500
57	ctgatgttcc gcagcggcgg cgcgtcttcc gtgcgcgggt acgaactcga cagcatcgga	1560
58	cttgccggcc cgaacggatc ggtcctgccc gaacgcgccc tcctgggtgg cagcctggaa	1620
59	taccaactgc cgtttacgcg caccctttcc ggcgcgggtg tccacgatat gggcgatgcc	1680
60	gccgcccaatt tcaaacgtat gaagctgaaa cacggttcgg gactgggcgt gcgctggttc	1740

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61 agcccgcttg cgccgttttc cttcgacatc gcctacgggc acagcgataa gaaaatccgc      1800
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64 <210> SEQ ID NO: 2
65 <211> LENGTH: 609
66 <212> TYPE: PRT
67 <213> ORGANISM: Neisseria meningitidis
69 <400> SEQUENCE: 2
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71 1 5 10 15
72 Pro His Ala Tyr Ala Pro Ala Ala Asp Leu Ser Glu Asn Lys Ala Ala
73 20 25 30
74 Gly Phe Ala Leu Phe Lys Asn Lys Ser Pro Asp Thr Glu Ser Val Lys
75 35 40 45
76 Leu Lys Pro Lys Phe Pro Val Arg Ile Asp Thr Gln Asp Ser Glu Ile
77 50 55 60
78 Lys Asp Met Val Glu Glu His Leu Pro Leu Ile Thr Gln Gln Gln Glu
79 65 70 75 80
80 Glu Val Leu Asp Lys Glu Gln Thr Gly Phe Leu Ala Glu Glu Ala Pro
81 85 90 95
82 Asp Asn Val Lys Thr Met Leu Arg Ser Lys Gly Tyr Phe Ser Ser Lys
83 100 105 110
84 Val Ser Leu Thr Glu Lys Asp Gly Ala Tyr Thr Val His Ile Thr Pro
85 115 120 125
86 Gly Pro Arg Thr Lys Ile Ala Asn Val Gly Val Ala Ile Leu Gly Asp
87 130 135 140
88 Ile Leu Ser Asp Gly Asn Leu Ala Glu Tyr Tyr Arg Asn Ala Leu Glu
89 145 150 155 160
90 Asn Trp Gln Gln Pro Val Gly Ser Asp Phe Asp Gln Asp Ser Trp Glu
91 165 170 175
92 Asn Ser Lys Thr Ser Val Leu Gly Ala Val Thr Arg Lys Gly Tyr Pro
93 180 185 190
94 Leu Ala Lys Leu Gly Asn Thr Arg Ala Ala Val Asn Pro Asp Thr Ala
95 195 200 205
96 Thr Val Asp Leu Asn Val Val Val Asp Ser Gly Arg Pro Ile Ala Phe
97 210 215 220
98 Gly Asp Phe Glu Ile Thr Gly Thr Gln Arg Tyr Pro Glu Gln Ile Val
99 225 230 235 240
100 Ser Gly Leu Ala Arg Phe Gln Pro Gly Thr Pro Tyr Asp Leu Asp Leu
101 245 250 255
102 Leu Leu Asp Phe Gln Gln Ala Leu Glu Gln Asn Gly His Tyr Ser Gly
103 260 265 270
104 Ala Ser Val Gln Ala Asp Phe Asp Arg Leu Gln Gly Asp Arg Val Pro
105 275 280 285
106 Val Lys Val Ser Val Thr Glu Val Lys Arg His Lys Leu Glu Thr Gly
107 290 295 300
108 Ile Arg Leu Asp Ser Glu Tyr Gly Leu Gly Gly Lys Ile Ala Tyr Asp
109 305 310 315 320
110 Tyr Tyr Asn Leu Phe Asn Lys Gly Tyr Ile Gly Ser Val Val Trp Asp
111 325 330 335

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112 Met Asp Lys Tyr Glu Thr Thr Leu Ala Ala Gly Ile Ser Gln Pro Arg
113           340           345           350
114 Asn Tyr Arg Gly Asn Tyr Trp Thr Ser Asn Val Ser Tyr Asn Arg Ser
115           355           360           365
116 Thr Thr Gln Asn Leu Glu Lys Arg Ala Phe Ser Gly Gly Ile Trp Tyr
117           370           375           380
118 Val Arg Asp Arg Ala Gly Ile Asp Ala Arg Leu Gly Ala Glu Phe Leu
119 385           390           395           400
120 Ala Glu Gly Arg Lys Ile Pro Gly Ser Asp Ile Asp Leu Gly Asn Ser
121           405           410           415
122 His Ala Thr Met Leu Thr Ala Ser Trp Lys Arg Gln Leu Leu Asn Asn
123           420           425           430
124 Val Leu His Pro Glu Asn Gly His Tyr Leu Asp Gly Lys Ile Gly Thr
125           435           440           445
126 Thr Leu Gly Thr Phe Leu Ser Thr Ala Leu Ile Arg Thr Ser Ala
127           450           455           460
128 Arg Ala Gly Tyr Phe Phe Thr Pro Glu Asn Lys Lys Leu Gly Thr Phe
129 465           470           475           480
130 Ile Ile Arg Gly Gln Ala Gly Tyr Thr Val Ala Arg Asp Asn Ala Asp
131           485           490           495
132 Val Pro Ser Gly Leu Met Phe Arg Ser Gly Gly Ala Ser Ser Val Arg
133           500           505           510
134 Gly Tyr Glu Leu Asp Ser Ile Gly Leu Ala Gly Pro Asn Gly Ser Val
135           515           520           525
136 Leu Pro Glu Arg Ala Leu Leu Val Gly Ser Leu Glu Tyr Gln Leu Pro
137           530           535           540
138 Phe Thr Arg Thr Leu Ser Gly Ala Val Phe His Asp Met Gly Asp Ala
139 545           550           555           560
140 Ala Ala Asn Phe Lys Arg Met Lys Leu Lys His Gly Ser Gly Leu Gly
141           565           570           575
142 Val Arg Trp Phe Ser Pro Leu Ala Pro Phe Ser Phe Asp Ile Ala Tyr
143           580           585           590
144 Gly His Ser Asp Lys Lys Ile Arg Trp His Ile Ser Leu Gly Thr Arg
145           595           600           605

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146 Phe

149 <210> SEQ ID NO: 3

150 <211> LENGTH: 1830

151 <212> TYPE: DNA

152 <213> ORGANISM: Neisseria meningitidis

154 <400> SEQUENCE: 3

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155 atgatgatca aaccgaccgc cctgctcctg ccggctttat ttttctttcc gcacgcatac      60
156 ggcctgccc cgcaccttc cgaaaacaag gcggcgggtt tcgcattgtt caaaaacaaa      120
157 agccccgaca ccgaatcagt taaattaaaa cccaaattcc ccgtccgcat cgacacgcag      180
158 gatagtgaat tcaaagatat ggtcgaagaa cacctgccgc tcatcacgca gcagcaggaa      240
159 gaagtattgg acaaggaaca gacgggcttc ctgcgccgaag aagcaccgga caacgttaaa      300
160 accatgctcc gcagcaaagg ctatttcagc agcaaagtca gcctgacgga aaaagacgga      360
161 gcttatacgg tacacatcac accgggcccc cgcacaaaaa tcgccaacgt cgggtgtcgc      420
162 atcctcggcg acatcctttc agacggcaac ctgcgccgaat actaccgcaa cgcgctggaa      480
163 aactggcagc agccggtagg cagtgatctc gatcaggaca gttgggaaaa cagcaaaact      540

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164 tccgtcctcg gcgcggtaac gcgcaaaggc taccgcgttg ccaagctcgg caacacccgg 600
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166 cccatcgctt tcggcgactt tgaaatcacc ggcacacagc gttaccccg acaaatcgtc 720
167 tccggcctgg cgcgcttcca accgggcacg ccctacgacc tcgacctgct gctcgacttc 780
168 caacaggcac tcgaacaaaa cgggcattat tccggcgctt ccgtacaagc cgacttcgac 840
169 cgtctccaag gcgaccgctt ccccgctcaa gtcagcgtaa ccgaggtcaa acgccacaag 900
170 ctcgaaaccg gcatccgctt cgattcggaa tacggtttgg gcggcaaaat cgcctacgac 960
171 tattacaacc tcttcaacaa aggtatatc ggctcggctg tctgggatat ggacaaatat 1020
172 gaaaccacgc ttgcgcgcgg catcagccag ccgcgcaact atcggggcaa ctactggaca 1080
173 agcaacgttt cctacaaccg ttcgaccacc caaaacctcg aaaaacgcgc cttctccggc 1140
174 ggcatctggt atgtgcgcga ccgcgcgggc atcgatgcca ggctgggggc agagtttctc 1200
175 gcagaaggcc ggaaaatccc cggtcgggat atcgatttgg gcaacagcca cgccacgatg 1260
176 ctgaccgcct cttggaaacg ccagctgctc aacaacgtgc tgcattccga aaacggccat 1320
177 tacctcgacg gcaaaatcgg tacgactttg ggcacattcc tgctctccac cgcgctgac 1380
178 cgcacctctg cccgtgcagg ttattttctt acgcccga aaacaaaaact cggcacgttc 1440
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180 ctgatgttcc gcagcggcgg cgcgtcttcc gtgcgcggtt acgaactcga cagcatcgga 1560
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183 gccgccaatt tcaaacgtat gaagctgaaa cacggttcgg gactgggcgt gcgctggtc 1740
184 agcccgcttg cgcggttttc cttcgacatc gcctacgggc acagcgataa gaaaatccgc 1800
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187 <210> SEQ ID NO: 4

188 <211> LENGTH: 609

189 <212> TYPE: PRT

190 <213> ORGANISM: Neisseria meningitidis

192 <400> SEQUENCE: 4

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195 Pro His Ala Tyr Ala Pro Ala Ala Asp Leu Ser Glu Asn Lys Ala Ala
196 20 25 30
197 Gly Phe Ala Leu Phe Lys Asn Lys Ser Pro Asp Thr Glu Ser Val Lys
198 35 40 45
199 Leu Lys Pro Lys Phe Pro Val Arg Ile Asp Thr Gln Asp Ser Glu Ile
200 50 55 60
201 Lys Asp Met Val Glu Glu His Leu Pro Leu Ile Thr Gln Gln Gln Glu
202 65 70 75 80
203 Glu Val Leu Asp Lys Glu Gln Thr Gly Phe Leu Ala Glu Glu Ala Pro
204 85 90 95
205 Asp Asn Val Lys Thr Met Leu Arg Ser Lys Gly Tyr Phe Ser Ser Lys
206 100 105 110
207 Val Ser Leu Thr Glu Lys Asp Gly Ala Tyr Thr Val His Ile Thr Pro
208 115 120 125
209 Gly Pro Arg Thr Lys Ile Ala Asn Val Gly Val Ala Ile Leu Gly Asp
210 130 135 140
211 Ile Leu Ser Asp Gly Asn Leu Ala Glu Tyr Tyr Arg Asn Ala Leu Glu
212 145 150 155 160
213 Asn Trp Gln Gln Pro Val Gly Ser Asp Phe Asp Gln Asp Ser Trp Glu
214 165 170 175

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217 Leu Ala Lys Leu Gly Asn Thr Arg Ala Ala Val Asn Pro Asp Thr Ala
218          195          200          205
219 Thr Val Asp Leu Asn Val Val Val Asp Ser Gly Arg Pro Ile Ala Phe
220          210          215          220
221 Gly Asp Phe Glu Ile Thr Gly Thr Gln Arg Tyr Pro Glu Gln Ile Val
222 225          230          235          240
223 Ser Gly Leu Ala Arg Phe Gln Pro Gly Thr Pro Tyr Asp Leu Asp Leu
224          245          250          255
225 Leu Leu Asp Phe Gln Gln Ala Leu Glu Gln Asn Gly His Tyr Ser Gly
226          260          265          270
227 Ala Ser Val Gln Ala Asp Phe Asp Arg Leu Gln Gly Asp Arg Val Pro
228          275          280          285
229 Val Lys Val Ser Val Thr Glu Val Lys Arg His Lys Leu Glu Thr Gly
230          290          295          300
231 Ile Arg Leu Asp Ser Glu Tyr Gly Leu Gly Gly Lys Ile Ala Tyr Asp
232 305          310          315          320
233 Tyr Tyr Asn Leu Phe Asn Lys Gly Tyr Ile Gly Ser Val Val Trp Asp
234          325          330          335
235 Met Asp Lys Tyr Glu Thr Thr Leu Ala Ala Gly Ile Ser Gln Pro Arg
236          340          345          350
237 Asn Tyr Arg Gly Asn Tyr Trp Thr Ser Asn Val Ser Tyr Asn Arg Ser
238          355          360          365
239 Thr Thr Gln Asn Leu Glu Lys Arg Ala Phe Ser Gly Gly Ile Trp Tyr
240          370          375          380
241 Val Arg Asp Arg Ala Gly Ile Asp Ala Arg Leu Gly Ala Glu Phe Leu
242 385          390          395          400
243 Ala Glu Gly Arg Lys Ile Pro Gly Ser Asp Ile Asp Leu Gly Asn Ser
244          405          410          415
245 His Ala Thr Met Leu Thr Ala Ser Trp Lys Arg Gln Leu Leu Asn Asn
246          420          425          430
247 Val Leu His Pro Glu Asn Gly His Tyr Leu Asp Gly Lys Ile Gly Thr
248          435          440          445
249 Thr Leu Gly Thr Phe Leu Ser Ser Thr Ala Leu Ile Arg Thr Ser Ala
250          450          455          460
251 Arg Ala Gly Tyr Phe Phe Thr Pro Glu Asn Lys Lys Leu Gly Thr Phe
252 465          470          475          480
253 Ile Ile Arg Gly Gln Ala Gly Tyr Thr Val Ala Arg Asp Asn Ala Asp
254          485          490          495
255 Val Pro Ser Gly Leu Met Phe Arg Ser Gly Gly Ala Ser Ser Val Arg
256          500          505          510
257 Gly Tyr Glu Leu Asp Ser Ile Gly Leu Ala Gly Pro Asn Gly Ser Val
258          515          520          525
259 Leu Pro Glu Arg Ala Leu Leu Val Gly Ser Leu Glu Tyr Gln Leu Pro
260          530          535          540
261 Phe Thr Arg Thr Leu Ser Gly Ala Val Phe His Asp Met Gly Asp Ala
262 545          550          555          560
263 Ala Ala Asn Phe Lys Arg Met Lys Leu Lys His Gly Ser Gly Leu Gly

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VERIFICATION SUMMARY

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date